

SEQUENCE LISTING

<110> Basi, Guriq
Saldanha, Jose
Yednock, Ted

<120> Humanized Antibodies that Recognize
Beta-Amyloid Peptide

<130> ELN-002

<150> 60/251,892

<151> 2000-12-06

<160> 63

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 396

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1)...(396)

<221> sig_peptide

<222> (1)...(60)

<400> 1

atg atg agt cct gcc cag ttc ctg ttt ctg tta gtg ctc tgg att cgg	48
Met Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Val Leu Trp Ile Arg	
-20 -15 -10 -5	
gaa acc aac ggt tat gtt gtg atg acc cag act cca ctc act ttg tcg	96
Glu Thr Asn Gly Tyr Val Val Met Thr Gln Thr Pro Leu Thr Leu Ser	
1 5 10	
gtt acc att gga caa cca gcc tcc atc tct tgc aag tca agt cag agc	144
Val Thr Ile Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser	
15 20 25	
ctc tta gat agt gat gga aag aca tat ttg aat tgg ttg tta cag agg	192
Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg	
30 35 40	
cca ggc cag tct cca aag cgc cta atc tat ctg gtg tct aaa ctg gac	240
Pro Gly Gln Ser Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp	
45 50 55 60	
tct gga gtc cct gac agg ttc act ggc agt gga tca ggg aca gat ttt	288
Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe	
65 70 75	

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<210> 2
<211> 132
<212> PRT
<213> Mus musculus
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<220>
<221> SIGNAL
<222> (1) ... (20)
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<400> 2
Met Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Val Leu Trp Ile Arg
-20                               -15                -10                -5
Glu Thr Asn Gly Tyr Val Val Met Thr Gln Thr Pro Leu Thr Leu Ser
                               1                      5                      10
Val Thr Ile Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser
                               15                20                25
Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg
                               30                35                40
Pro Gly Gln Ser Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp
45                               50                55                60
Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe
                               65                70                75
Thr Leu Lys Ile Ser Arg Ile Glu Ala Glu Asp Leu Gly Leu Tyr Tyr
                               80                85                90
Cys Trp Gln Gly Thr His Phe Pro Arg Thr Phe Gly Gly Gly Thr Lys
                               95                100               105
Leu Glu Ile Lys
110

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<210> 3
<211> 414
<212> DNA
<213> Mus musculus
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<220>
<221> CDS
<222> (1) ... (414)
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<221> sig_peptide
<222> (1)...(57)
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<400> 3
 atg aac ttc ggg ctc agc ttg att ttc ctt gtc ctt gtt tta aaa ggt 48
 Met Asn Phe Gly Leu Ser Leu Ile Phe Leu Val Leu Val Leu Lys Gly
 -15 -10 -5

gtc cag tgt gaa gtg aag ctg gtg gag tct ggg gga ggc tta gtg aag 96
 Val Gln Cys Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Lys
 1 5 10

cct gga gcg tct ctg aaa ctc tcc tgt gca gcc tct gga ttc act ttc 144
 Pro Gly Ala Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
 15 20 25

agt aac tat ggc atg tct tgg gtt cgc cag aat tca gac aag agg ctg 192
 Ser Asn Tyr Gly Met Ser Trp Val Arg Gln Asn Ser Asp Lys Arg Leu
 30 35 40 45

gag tgg gtt gca tcc att agg agt ggt ggt ggt aga acc tac tat tca 240
 Glu Trp Val Ala Ser Ile Arg Ser Gly Gly Gly Arg Thr Tyr Tyr Ser
 50 55 60

gac aat gta aag ggc cga ttc acc atc tcc aga gag aat gcc aag aac 288
 Asp Asn Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Ala Lys Asn
 65 70 75

acc ctg tac ctg caa atg agt agt ctg aag tct gag gac acg gcc ttg 336
 Thr Leu Tyr Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Leu
 80 85 90

tat tat tgt gtc aga tat gat cac tat agt ggt agc tcc gac tac tgg 384
 Tyr Tyr Cys Val Arg Tyr Asp His Tyr Ser Gly Ser Ser Asp Tyr Trp
 95 100 105

ggc cag ggc acc act gtc aca gtc tcc tca 414
 Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 110 115

<210> 4
 <211> 138
 <212> PRT
 <213> Mus musculus

<220>
 <221> SIGNAL
 <222> (1)...(19)

<400> 4
 Met Asn Phe Gly Leu Ser Leu Ile Phe Leu Val Leu Val Leu Lys Gly
 -15 -10 -5
 Val Gln Cys Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Lys
 1 5 10
 Pro Gly Ala Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
 15 20 25
 Ser Asn Tyr Gly Met Ser Trp Val Arg Gln Asn Ser Asp Lys Arg Leu
 30 35 40 45

<400> 6

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Met Gly Leu Leu Met Leu Trp Val Ser Gly Ser Ser Gly Asp Ile Val
      -15      -10      -5
Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly Glu Pro Ala
      1      5      10
Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr
      15      20      25
Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu
      30      35      40      45
Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe
      50      55      60
Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val
      65      70      75
Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala Leu Gln Thr
      80      85      90
Pro Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
      95      100      105

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<210> 7
<211> 100
<212> PRT
<213> Homo sapiens

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<400> 7
Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
      1      5      10      15
Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
      20      25      30
Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
      35      40      45
Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro
      50      55      60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
      65      70      75      80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
      85      90      95
Leu Gln Thr Pro
      100

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<210> 8
<211> 138
<212> PRT
<213> Artificial Sequence

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<220>
<223> Humanized 3D6 heavy chain variable region

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<221> SIGNAL
<222> (1)...(19)

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<400> 8
Met Asn Phe Gly Leu Ser Leu Ile Phe Leu Val Leu Val Leu Lys Gly
      -15      -10      -5
Val Gln Cys Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln
      1      5      10

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Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
   15           20           25
Ser Asn Tyr Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 30           35           40           45
Glu Trp Val Ala Ser Ile Arg Ser Gly Gly Gly Arg Thr Tyr Tyr Ser
           50           55           60
Asp Asn Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
           65           70           75
Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu
           80           85           90
Tyr Tyr Cys Val Arg Tyr Asp His Tyr Ser Gly Ser Ser Asp Tyr Trp
           95          100          105
Gly Gln Gly Thr Leu Val Thr Val Ser Ser
110           115

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<210> 9
<211> 121
<212> PRT
<213> Homo sapiens

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<400> 9
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1           5           10           15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
           20           25           30
Ala Val Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
           35           40           45
Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
           50           55           60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
 65           70           75           80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
           85           90           95
Ala Lys Asp Asn Tyr Asp Phe Trp Ser Gly Thr Phe Asp Tyr Trp Gly
           100          105          110
Gln Gly Thr Leu Val Thr Val Ser Ser
115           120

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<210> 10
<211> 98
<212> PRT
<213> Homo sapiens

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<400> 10
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
           20           25           30
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
           35           40           45
Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
           50           55           60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65           70           75           80

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Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Lys

<210> 11
 <211> 132
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> SIGNAL
 <222> (1)...(20)

<223> humanized 3D6 light chain variable region

<400> 11
 Met Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Val Leu Trp Ile Arg
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 Glu Thr Asn Gly Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro
 1 5 10
 Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser
 15 20 25
 Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Lys
 30 35 40
 Pro Gly Gln Ser Pro Gln Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp
 45 50 55 60
 Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
 65 70 75
 Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
 80 85 90
 Cys Trp Gln Gly Thr His Phe Pro Arg Thr Phe Gly Gln Gly Thr Lys
 95 100 105
 Val Glu Ile Lys
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<210> 12
 <211> 138
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanized 3D6 light chain variable region

<221> SIGNAL
 <222> (1)...(19)

<400> 12
 Met Asn Phe Gly Leu Ser Leu Ile Phe Leu Val Leu Val Leu Lys Gly
 -15 -10 -5
 Val Gln Cys Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln
 1 5 10
 Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
 15 20 25

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Ser Asn Tyr Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
30          35          40          45
Glu Trp Val Ala Ser Ile Arg Ser Gly Gly Gly Arg Thr Tyr Tyr Ser
          50          55          60
Asp Asn Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
          65          70          75
Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
          80          85          90
Tyr Tyr Cys Val Arg Tyr Asp His Tyr Ser Gly Ser Ser Asp Tyr Trp
          95          100          105
Gly Gln Gly Thr Leu Val Thr Val Ser Ser
110          115

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<210> 13
 <211> 393
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)...(393)
 <221> sig_peptide
 <222> (1)...(57)

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<400> 13
atg aag ttg cct gtt agg ctg ttg gta ctg atg ttc tgg att cct gct 48
Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile Pro Ala
          -15          -10          -5

tcc agc agt gat gtt ttg atg acc caa act cca ctc tcc ctg cct gtc 96
Ser Ser Ser Asp Val Leu Met Thr Gln Thr Pro Leu Ser Leu Pro Val
          1          5          10

agt ctt gga gat caa gcc tcc atc tct tgc aga tct agt cag aac att 144
Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Asn Ile
          15          20          25

ata cat agt aat gga aac acc tat tta gaa tgg tac ctg cag aaa cca 192
Ile His Ser Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro
          30          35          40          45

ggc cag tct cca aag ctc ctg atc tac aaa gtt tcc aac cga ttt tct 240
Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser
          50          55          60

ggg gtc cca gac agg ttc agt ggc agt gga tca ggg aca gat ttc aca 288
Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
          65          70          75

ctc aag atc aag aaa gtg gag gct gag gat ctg gga att tat tac tgc 336
Leu Lys Ile Lys Lys Val Glu Ala Glu Asp Leu Gly Ile Tyr Tyr Cys
          80          85          90

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gag ctg gaa
Glu Leu Glu
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<220>  
<221> SIGNAL  
<222> (1) ... (19)
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<220>  
<221> CDS  
<222> (1) . . . (426)
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<400> 15
atg gac agg ctt act tcc tca ttc ctg ctg ctg att gtc cct gca tat 48
Met Asp Arg Leu Thr Ser Ser Phe Leu Leu Leu Ile Val Pro Ala Tyr
          -15                -10                -5

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gtc ctg tcc cag gct act ctg aaa gag tct ggc cct gga ata ttg cag 96
Val Leu Ser Gln Ala Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu Gln
      1              5              10

tcc tcc cag acc ctc agt ctg act tgt tct ttc tct ggg ttt tca ctg 144
Ser Ser Gln Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu
      15              20              25

agc act tct ggt atg gga gtg agc tgg att cgt cag cct tca gga aag 192
Ser Thr Ser Gly Met Gly Val Ser Trp Ile Arg Gln Pro Ser Gly Lys
      30              35              40              45

ggg ctg gag tgg ctg gca cac att tac tgg gat gat gac aag cgc tat 240
Gly Leu Glu Trp Leu Ala His Ile Tyr Trp Asp Asp Asp Lys Arg Tyr
      50              55              60

aac cca tcc ctg aag agc cgg ctc aca atc tcc aag gat acc tcc aga 288
Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Arg
      65              70              75

aag cag gta ttc ctc aag atc acc agt gtg gac cct gca gat act gcc 336
Lys Gln Val Phe Leu Lys Ile Thr Ser Val Asp Pro Ala Asp Thr Ala
      80              85              90

aca tac tac tgt gtt cga agg ccc att act ccg gta cta gtc gat gct 384
Thr Tyr Tyr Cys Val Arg Arg Pro Ile Thr Pro Val Leu Val Asp Ala
      95              100              105

atg gac tac tgg ggt caa gga acc tca gtc acc gtc tcc tca 426
Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
      110              115              120

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<210> 16
 <211> 142
 <212> PRT
 <213> Mus musculus

<220>
 <221> SIGNAL
 <222> (1)...(19)

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<400> 16
Met Asp Arg Leu Thr Ser Ser Phe Leu Leu Leu Ile Val Pro Ala Tyr
      -15              -10              -5
Val Leu Ser Gln Ala Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu Gln
      1              5              10
Ser Ser Gln Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu
      15              20              25
Ser Thr Ser Gly Met Gly Val Ser Trp Ile Arg Gln Pro Ser Gly Lys
      30              35              40              45
Gly Leu Glu Trp Leu Ala His Ile Tyr Trp Asp Asp Asp Lys Arg Tyr
      50              55              60
Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Arg
      65              70              75
Lys Gln Val Phe Leu Lys Ile Thr Ser Val Asp Pro Ala Asp Thr Ala

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<220>
<223> Primer

[illegible]

<400> 20
aattctagga tccactcacg cttgatctcc accttgggtgc cctggccgaa ggtgcggggg 60
aagtgggtgc cctgccagca gtagtacacg cccacgtcct cggcctccac gcgggagatc 120
ttcagggtga agtcggtgcc gg 142

<210> 21
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 21
ctgggggggac tggccg 16

<210> 22
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 22
acctgaactg gctgctgcag aa 22

<210> 23
<211> 138
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 23
acagaaagct tgccgccacc atggagtttg ggctgagctg gctttttctt gtggctatatt 60
taaaaggtgt ccagtgtgag gtgcagctgc tggagtcagg cggcggcctg gtgcagcccg 120
gcggctccct gcgcctgt 138

<210> 24
<211> 135
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 24
gccgccggag cggatggagg ccaccactc caggcccttg ccgggggcct ggcgcaccca 60
ggacatgccg tagttggaga aggtgaagcc ggaggcggcg caggacaggc gcaggagacc 120
gccgggctgc accag 135

<210> 25
<211> 142
<212> DNA
<213> Artificial Sequence

1001094-1001094

<223> Primer

ctggagtgagg	tgccctccat	ccgctccggc	ggcggccgca	cctactactc	cgacaacgtg	60
aagggcgcgct	tcaccatctc	ccgcgacaac	gccagaact	ccctgtacct	gcagatgaac	120
tccctgcccgc	ccgaggacac	cg				142

<211> 144

<213> Artificial Sequence

<223> Primer

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ctgcaaggat ccactcacgg gaggacacggg tcaccagggt gccctggccc cagtagtcgg 60
aggagccgga gtagtggtcg tagcgcacgc agtagtacag ggcggtgtcc tcggcgcgca 120
gggagttcat ctgcaggtac aggg                                     144

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<211> 16

<213> Artificial Sequence

<223> Primer

gccgccggag cggatg 16

<211> 20

<213> Artificial Sequence

<223> Primer

ctggagtggg tggcctccat 20

<211> 19

<213> Artificial Sequence

<223> Primer

tccgcaagct tgccgccac

<210> 30
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 30
aattctagga tccactcacg cttgatctc

29

<210> 31
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 31
acagaaagct tgccgccacc atg

23

<210> 32
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 32
ctgcaaggat ccactcaccg ga

22

<210> 33
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> internal peptide

<400> 33
Asp Ala Glu Phe Arg His Asp Ser Gly Tyr
1 5 10

<210> 34
<211> 402
<212> DNA
<213> Artificial Sequence

<220>
<223> h3D6 version 1 VL

<400> 34
 atggacatgc gcgtagccgc ccagctgctg ggctgctga tgctgtgggt gtccggctcc 60
 tccgggtacg tggtagatgac ccagtcctcc ctgtccctgc ccgtgacccc cggcgagccc 120
 gcctccatct cctgcaagtc ctcccagtc ctgtgtgact ccgacggcaa gacctacctg 180
 aactggctgc tgcagaagcc cggccagtc cccagcgcc tgatctacct ggtgtccaag 240
 ctggactccg gcgtagccga ccgcttctcc ggctccggct ccggcaccga cttcacctg 300
 aagatctccc gcgtaggagc cgaggacgtg ggctgtact actgctggca gggcacccac 360
 tcccccgca ccttcggcca gggcaccaag gtggagatca ag 402

<210> 35
 <211> 402
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> h3D6 version 2 VL

<400> 35
 atggacatgc gcgtagccgc ccagctgctg ggctgctga tgctgtgggt gtccggctcc 60
 tccggcgacg tggtagatgac ccagtcctcc ctgtccctgc ccgtgacccc cggcgagccc 120
 gcctccatct cctgcaagtc ctcccagtc ctgtgtgact ccgacggcaa gacctacctg 180
 aactggctgc tgcagaagcc cggccagtc cccagcgcc tgatctacct ggtgtccaag 240
 ctggactccg gcgtagccga ccgcttctcc ggctccggct ccggcaccga cttcacctg 300
 aagatctccc gcgtaggagc cgaggacgtg ggctgtact actgctggca gggcacccac 360
 tcccccgca ccttcggcca gggcaccaag gtggagatca ag 402

<210> 36
 <211> 414
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> h3D6 version 1 VH

<400> 36
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 gtgcagctgc tggagtccgg cggcggcctg gtgcagcccg gcggctccct gcgcctgtcc 120
 tgcgcgcct ccggcttcac cttctccaac tacggcatgt cctgggtgcg ccaggccccc 180
 ggcaaggggc tggagtgggt ggctccatc cgctccggcg gcggccgcac ctactactcc 240
 gacaacgtga agggccgctt caccatctcc cgcgacaacg ccaagaactc cctgtacctg 300
 cagatgaact ccctgcgcgc cgaggacacc gccctgtact actgcgtgcg ctacgaccac 360
 tactccggct cctccgacta ctggggccag ggcacctgg tgacctgtc ctcc 414

<210> 37
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 <213> Artificial Sequence

<220>
 <223> h3D6 version 2 VH

<400> 37
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 gtgcagctgc tggagtccgg cggcggcctg gtgcagcccg gcggctccct gcgcctgtcc 120
 tgcgcgcct ccggcttcac cttctccaac tacggcatgt cctgggtgcg ccaggccccc 180
 ggcaaggggc tggagtgggt ggctccatc cgctccggcg gcggccgcac ctactactcc 240
 gacaacgtga agggccgctt caccatctcc cgcgacaact ccaagaacac cctgtacctg 300

004094 2460700

cagatgaact cctgcgcgc cgaggacacc gccgtgtact actgcgtgcg ctacgaccac 360
tactccggct cctccgacta ctggggccag ggcaccctgg tgaccgtgtc

<210> 38
<211> 770
<212> PRT
<213> Homo Sapiens

<400> 38
Met Leu Pro Gly Leu Ala Leu Leu Leu Leu Ala Ala Trp Thr Ala Arg
1 5 10 15
Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro
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Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
35 40 45
Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
50 55 60
Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
65 70 75 80
Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
85 90 95
Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
100 105 110
Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
115 120 125
Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
130 135 140
Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
145 150 155 160
Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
165 170 175
Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
180 185 190
Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
195 200 205
Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
210 215 220
Val Val Glu Val Ala Glu Glu Glu Val Ala Glu Val Glu Glu Glu
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Cys Met Ala Val Cys Gly Ser Ala Met Ser Gln Ser Leu Leu Lys Thr
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